

SEQUENCE LISTING

(1) GENERAL INFORMATION

(i) APPLICANT: Hillman, Jennifer L.
Tang, Y. Tom
Lal, Preeti
Guegler, Karl J.
Corley, Neil C.
Patterson, Chandra
Batra, Sajeev
Baughn, Mariah R.

(ii) TITLE OF THE INVENTION: RAS PROTEINS

(iii) NUMBER OF SEQUENCES: 14

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
(B) STREET: 3174 Porter Drive
(C) CITY: Palo Alto
(D) STATE: CA
(E) COUNTRY: US

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: Word Perfect 6.1/MS-DOS 6.2

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: To Be Assigned
(B) FILING DATE: Herewith
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: 08/766,551
(B) FILING DATE: DECEMBER 12, 1996

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Cerrone, Michael C.
(B) REGISTRATION NUMBER: 39,132
(C) REFERENCE/DOCKET NUMBER: PF-0168-1 CIP

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 650-855-0555
(B) TELEFAX: 650-845-4166
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

PF-0168-3 DIV

- (A) LENGTH: 259 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNNOT05
- (B) CLONE: 627565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1 :

Met Asn Ile Leu Ala Pro Val Arg Arg Asp Arg Val Leu Ala Glu
5 10 15
Leu Pro Gln Cys Leu Arg Lys Glu Ala Ala Leu His Gly His Lys
20 25 30
Asp Phe His Pro Arg Val Thr Cys Ala Cys Gln Glu His Arg Thr
35 40 45
Gly Thr Val Gly Phe Lys Ile Ser Lys Val Ile Val Val Gly Asp
50 55 60
Leu Ser Val Gly Lys Thr Cys Leu Ile Asn Arg Phe Cys Lys Asp
65 70 75
Thr Phe Asp Lys Asn Tyr Lys Ala Thr Ile Gly Val Asp Phe Glu
80 85 90
Met Glu Arg Phe Glu Val Leu Gly Ile Pro Phe Ser Leu Gln Leu
95 100 105
Trp Asp Thr Ala Gly Gln Glu Arg Phe Lys Cys Ile Ala Ser Thr
110 115 120
Tyr Tyr Arg Gly Ala Gln Ala Ile Ile Ile Val Phe Asn Leu Asn
125 130 135
Asp Val Ala Ser Leu Glu His Thr Lys Gln Trp Leu Ala Asp Ala
140 145 150
Leu Lys Glu Asn Asp Pro Ser Ser Val Leu Leu Phe Leu Val Gly
155 160 165
Ser Lys Lys Asp Leu Ser Thr Pro Ala Gln Tyr Ala Leu Met Glu
170 175 180
Lys Asp Ala Leu Gln Val Ala Gln Glu Met Lys Ala Glu Tyr Trp
185 190 195
Ala Val Ser Ser Leu Thr Gly Glu Asn Val Arg Glu Phe Phe
200 205 210
Arg Val Ala Ala Leu Thr Phe Glu Ala Asn Val Leu Ala Glu Leu
215 220 225
Glu Lys Ser Gly Ala Arg Arg Ile Gly Asp Val Val Arg Ile Asn
230 235 240
Ser Asp Asp Ser Asn Leu Tyr Leu Thr Ala Ser Lys Lys Lys Pro
245 250 255
Thr Cys Cys Pro

(2) INFORMATION FOR SEQ ID NO: 2:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 196 amino acids

PF-0168-3 DIV

- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: COLNOT05
 - (B) CLONE: 775601

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2 :

Met Gly Ile Leu Phe Thr Arg Ile Trp Arg Leu Phe Asn His Gln
5 10 15
Gly Pro Arg Gly Ser Ser Gln Thr Asn Ala Ala Ala Met Ser Ala
20 25 30
Ser Leu Glu His Lys Val Ile Ile Val Gly Leu Asp Asn Ala Gly
35 40 45
Lys Thr Thr Ile Leu Tyr Gln Phe Ser Met Asn Glu Val Val His
50 55 60
Thr Ser Pro Thr Ile Gly Gly Asn Val Glu Glu Ile Ala Ile Asn
65 70 75
Asn Thr Arg Phe Leu Met Trp Asp Ile Gly Gly Gln Glu Ser Leu
80 85 90
Arg Ser Ser Trp Asn Thr Tyr Tyr Thr Asn Thr Glu Phe Val Ile
95 100 105
Val Val Val Asp Ser Thr Asp Arg Glu Arg Ile Ser Val Thr Arg
110 115 120
Glu Glu Leu Tyr Lys Met Leu Ala His Glu Asp Pro Arg Lys Ala
125 130 135
Gly Leu Leu Ile Phe Ala Asn Lys Gln Asp Val Lys Glu Cys Met
140 145 150
Thr Val Ala Glu Ile Ser Gln Phe Leu Lys Leu Thr Ser Ile Lys
155 160 165
Asp His Gln Trp His Ile Gln Ala Cys Cys Ala Leu Thr Gly Glu
170 175 180
Gly Leu Cys Gln Gly Leu Glu Trp Met Met Ser Arg Leu Lys Ile
185 190 195
Arg

- (2) INFORMATION FOR SEQ ID NO: 3:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 191 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: UCMCL5T01
 - (B) CLONE: 1528559

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3 :

PF-0168-3 DIV

Met Leu Leu Gly Asp Thr Gly Val Gly Lys Thr Cys Phe Leu Ile
5 10 15
Gln Phe Lys Asp Gly Ala Phe Leu Ser Gly Thr Phe Ile Ala Thr
20 25 30
Val Gly Ile Asp Phe Arg Asn Lys Val Val Thr Val Asp Gly Val
35 40 45
Arg Val Lys Leu Gln Ile Trp Asp Thr Ala Gly Gln Glu Arg Phe
50 55 60
Arg Ser Val Thr His Ala Tyr Tyr Arg Asp Ala Gln Ala Leu Leu
65 70 75
Leu Leu Tyr Asp Ile Thr Asn Lys Ser Ser Phe Asp Asn Ile Arg
80 85 90
Ala Trp Leu Thr Glu Ile His Glu Tyr Ala Gln Arg Asp Val Val
95 100 105
Ile Met Leu Leu Gly Asn Lys Ala Asp Met Ser Ser Glu Arg Val
110 115 120
Ile Arg Ser Glu Asp Gly Glu Thr Leu Ala Arg Glu Tyr Gly Val
125 130 135
Pro Phe Leu Glu Thr Ser Ala Lys Thr Gly Met Asn Val Glu Leu
140 145 150
Ala Phe Leu Ala Ile Ala Lys Glu Leu Lys Tyr Arg Ala Gly His
155 160 165
Gln Ala Asp Glu Pro Ser Phe Gln Ile Arg Asp Tyr Val Glu Ser
170 175 180
Gln Lys Lys Arg Ser Ser Cys Cys Ser Phe Met
185 190

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 260 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: PROSTUT08
(B) CLONE: 1651593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4 :

Met Asn Ile Leu Ala Pro Val Arg Arg Asp Arg Val Leu Ala Glu
5 10 15
Leu Pro Gln Cys Leu Arg Lys Glu Ala Ala Leu His Gly His Lys
20 25 30
Asp Phe His Pro Arg Val Thr Cys Ala Cys Gln Glu His Arg Thr
35 40 45
Gly Thr Val Gly Arg Phe Lys Ile Ser Lys Val Ile Val Val Gly
50 55 60
Asp Leu Ser Val Gly Lys Thr Cys Leu Ile Asn Arg Phe Cys Lys
65 70 75

Asp Thr Phe Asp Lys Asn Tyr Lys Ala Thr Ile Gly Val Asp Phe
 80 85 90
 Glu Met Glu Arg Phe Glu Val Leu Gly Ile Pro Phe Ser Leu Gln
 95 100 105
 Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Lys Cys Ile Ala Ser
 110 115 120
 Thr Tyr Tyr Arg Gly Ala Gln Ala Ile Ile Ile Val Phe Asn Leu
 125 130 135
 Asn Asp Val Ala Ser Leu Glu His Thr Lys Gln Trp Leu Ala Asp
 140 145 150
 Ala Leu Lys Glu Asn Asp Pro Ser Ser Val Leu Leu Phe Leu Val
 155 160 165
 Gly Ser Lys Lys Asp Leu Ser Thr Pro Ala Gln Tyr Ala Leu Met
 170 175 180
 Glu Lys Asp Ala Leu Gln Val Ala Gln Glu Met Lys Ala Glu Tyr
 185 190 195
 Trp Ala Val Ser Ser Leu Thr Gly Glu Asn Val Arg Glu Phe Phe
 200 205 210
 Phe Arg Val Ala Ala Leu Thr Phe Glu Ala Asn Val Leu Ala Glu
 215 220 225
 Leu Glu Lys Ser Gly Ala Arg Arg Ile Gly Asp Val Val Arg Ile
 230 235 240
 Asn Ser Asp Asp Ser Asn Leu Tyr Leu Thr Ala Ser Lys Lys Lys
 245 250 255
 Pro Thr Cys Cys Pro
 260

1000549868 011500

(2) INFORMATION FOR SEQ ID NO: 5:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 190 amino acids
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: BLADNOT05
 - (B) CLONE: 1673056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5 :

Met Leu Pro Ile Phe Ile Ser Asn Trp Trp Leu Asp Met Leu Gly
 5 10 15
 Leu Val Trp Glu Pro Ser Asp Lys Leu Lys Gly Trp Ile Arg Lys
 20 25 30
 Arg Leu Thr Thr Pro Leu Val Ala Gly Gln Glu Asp Tyr Asp Arg
 35 40 45
 Leu Arg Thr Leu Ser Tyr Pro Gln Thr Val Gly Glu Thr Tyr Gly
 50 55 60
 Lys Asp Ile Thr Ser Arg Gly Lys Asp Met Pro Ile Ala Asp Val
 65 70 75

PF-0168-3 DIV

Phe Leu Ile Cys Phe Ser Leu Val Ser Pro Ala Ser Phe Glu Asn
80 85 90
Val Arg Ala Lys Trp Tyr Pro Glu Val Arg His His Cys Pro Asn
95 100 105
Thr Pro Ile Ile Leu Val Gly Thr Lys Leu Asp Leu Arg Asp Asp
110 115 120
Lys Asp Thr Ile Glu Lys Leu Lys Glu Lys Lys Leu Thr Pro Ile
125 130 135
Thr Tyr Pro Gln Gly Leu Ala Met Ala Lys Glu Ile Gly Ala Val
140 145 150
Lys Tyr Leu Glu Cys Ser Ala Leu Thr Gln Arg Gly Leu Lys Thr
155 160 165
Val Phe Asp Glu Ala Ile Arg Ala Val Ile Cys Pro Pro Pro Val
170 175 180
Lys Lys Arg Lys Arg Lys Cys Leu Met Leu
185 190

105514886 041502

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 211 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT10
- (B) CLONE: 2703745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6 :

Met Thr Thr Leu Asn Leu Leu Ala His Arg Arg Leu Thr Arg Leu
5 10 15
Tyr Leu Leu Gly Thr Leu Gln Trp Gly Ser Leu Val Ser Ser Trp
20 25 30
Arg Leu Cys Lys Asn Glu Phe Arg Glu Asn Ile Ser Ala Thr Leu
35 40 45
Gly Val Asp Phe Gln Met Lys Thr Leu Ile Val Asp Gly Glu Arg
50 55 60
Thr Val Leu Gln Leu Trp Asp Thr Ala Gly Gln Glu Arg Phe Arg
65 70 75
Ser Ile Ala Lys Ser Tyr Phe Arg Lys Ala Asp Gly Val Leu Leu
80 85 90
Leu Tyr Asp Val Thr Cys Glu Lys Ser Phe Leu Asn Ile Arg Glu
95 100 105
Trp Val Asp Met Ile Glu Asp Ala Ala His Glu Thr Val Pro Ile
110 115 120
Met Leu Val Gly Asn Lys Ala Asp Ile Arg Asp Thr Ala Ala Thr
125 130 135
Glu Gly Gln Lys Cys Val Pro Gly His Phe Gly Glu Lys Leu Ala
140 145 150

PF-0168-3 DIV

Met Thr Tyr Gly Ala Leu Phe Cys Glu Thr Ser Ala Lys Asp Gly
155 160 165
Ser Asn Ile Val Glu Ala Val Leu His Leu Ala Arg Glu Val Lys
170 175 180
Lys Arg Thr Asp Lys Asp Asp Ser Arg Ser Ile Thr Asn Leu Thr
185 190 195
Gly Thr Asn Ser Lys Lys Ser Pro Gln Met Lys Asn Cys Cys Asn
200 205 210
Gly

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 266 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENCNOT06
- (B) CLONE: 3440519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7 :

Met Ser Ser Val Phe Gly Lys Pro Arg Ala Gly Ser Gly Pro Gln
5 10 15
Ser Ala Pro Leu Glu Val Asn Leu Ala Ile Leu Gly Arg Arg Gly
20 25 30
Ala Gly Lys Ser Ala Leu Thr Val Lys Phe Leu Thr Lys Arg Phe
35 40 45
Ile Ser Glu Tyr Asp Pro Asn Leu Glu Asp Thr Tyr Ser Ser Glu
50 55 60
Glu Thr Val Asp His Gln Pro Val His Leu Arg Val Met Asp Thr
65 70 75
Ala Asp Leu Asp Thr Pro Arg Asn Cys Glu Arg Tyr Leu Asn Trp
80 85 90
Ala His Ala Phe Leu Val Val Tyr Ser Val Asp Ser Arg Gln Ser
95 100 105
Phe Asp Ser Ser Ser Tyr Leu Glu Leu Leu Ala Leu His Ala
110 115 120
Lys Glu Thr Gln Arg Ser Ile Pro Ala Leu Leu Leu Gly Asn Lys
125 130 135
Leu Asp Met Ala Gln Tyr Arg Gln Val Thr Lys Ala Glu Gly Val
140 145 150
Ala Leu Ala Gly Arg Phe Gly Cys Leu Phe Phe Glu Val Ser Ala
155 160 165
Cys Leu Asp Phe Glu His Val Gln His Val Phe His Glu Ala Val
170 175 180
Arg Glu Ala Arg Arg Glu Leu Glu Lys Ser Pro Leu Thr Arg Pro
185 190 195
Leu Phe Ile Ser Glu Glu Arg Ala Leu Pro His Gln Ala Pro Leu

PF-0168-3 DIV

200	205	210
Thr Ala Arg His Gly Leu Ala Ser Cys	Thr Phe Asn Thr Leu Ser	
215	220	225
Thr Ile Asn Leu Lys Glu Met Pro Thr Val Ala Gln Ala Lys Leu		
230	235	240
Val Thr Val Lys Ser Ser Arg Ala Gln Ser Lys Arg Lys Ala Pro		
245	250	255
Thr Leu Thr Leu Leu Lys Gly Phe Lys Ile Phe		
260	265	

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1172 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: KIDNNOT05
- (B) CLONE: 627565

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8 :

GGGCCCTGCAAGGCCAGGCAGGATGAA CATTCTGGCA CCCGTGCGGA GGGATCGCGT 60
CCTGGCGGAGCTGCCCCAGTGCCTGAGGAA GGAGGCCGCT TTGCACGGGC ACAAAGACTT 120
CCACCCCCCGCTCACCTGCG CCTGCCAGGA GCACCGGACA GGCACCGTGG GATTAAAGAT 180
CTCCAAGGTC ATTGTGGTGG GGGACCTGTC GGTGGGGAAAG ACTTGCCCTCA TTAATAGGTT 240
CTGAAAGAC ACCTTGATA AGAATTACAA GCCAACCATGGAGTGGACT TCGAGATGGA 300
ACGATTGAG GTGCTGGCA TTCCCTTCAG TTTGAGCTT TGGGATACCG CTGGGCAGGA 360
GAGGTTCAAATGCATTGCAT CAACCTACTA TAGAGGAGCT CAAGCCATCA TCATTGTCTT 420
CAACCTGAAT GATGTGGCAT CTCTGGAAACA TACCAAGCAG TGGCTGCCG ATGCCCTGAA 480
GGAGAATGAC CCTTCCAGTG TGCTTCTCTT CCTTGTAGGT TCCAAGAAGG ATCTGAGTAC 540
CCCTGCTCAG TATGCGCTGA TGGAGAAAGA CGCCCTCCAG GTGGCCCAGG AGATGAAGGC 600
TGAGTACTGG GCAGTCTCAT CTCTCACTGG TGAGAATGTC CGAGAATTCT TCTTCCGTGT 660
GGCAGCACTG ACCTTGAGG CCAATGTGCT GGCTGAGCTG GAGAAATCGG GGGCTCGACG 720
CATTGGGGAT GTTGTCCGCA TCAACAGTGA TGACAGCAAC CTCTACCTAA CTGCCAGCAA 780
GAAGAAGCCC ACATGTTGCC CATGAGGGCT GAGGAGACTG TTCAGAGACT GCCCAGCCCT 840
AGGGCACTGT GCCACCCCTCA TTCCCTCCAGA GCTTGACCCC TGGACATTG CACTGACTTT 900
ATCCAGACCA AAGAGCTGCC TCTTGGTGGC AGTATTCCCA CAGAGGGTA GCTGGGATCA 960
TGCTAGTCAC TTCCCTGCC CAGGCACCGT GCCAAAGACT GGATGCCCTT TACTCCTCAG 1020
GGGACTGTCC AGGGCGCCC GTGGTAGTGA GGGAGAGTGT CTCTGTTCTT TTGCTCAGCC 1080
TGCTGGGCCCTTGTGTTTG AGGATGCTTA ATGATTCCAG CCTCTCACTG TGCCTTATGC 1140
ATTAAAATTT CTTTGTACAG AGCAAAAAAA AA 1172

(2) INFORMATION FOR SEQ ID NO: 9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1469 base pairs
- (B) TYPE: nucleic acid

PF-0168-3 DIV

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: COLNNOT05
 - (B) CLONE: 775601

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 9 :

GAGCCAGGCG AGTGCAGCGG CGGAGCGCGG TGNCTTTGC GCGCGGNANG GGGCCTGGC 60
TTCGGCTCCC TCCGGTTCCC TGGAAGCGGG CCCNGACCAG NCGGAGCAGC AGCAGAGGCG 120
GAGNTCCAGC NGTCTCTCTC CTCCCCCTCA GCCTGAGCCG GGGGAANCAG NCGCCCGGGT 180
GTCTGGAGGG GGGGGGGTCC GCTGCCCGAG AATGGGAATT CTCTTCACTA GAATATGGAG 240
ACTGTTCAAT CACCAAGGGCC CGCGAGGCTC GTCCGAGACG AACCGGGCG CGATGTCCGC 300
GAGCCTAGAG CACAAAGTTA TCATTGTTGG GCTGGATAAT GCAGGGAAAA CTACCATTTCT 360
TTACCAATT TCTATGAACG AAGTTGTACA TACATCTCCT ACAATAGGAG GTAATGTAGA 420
AGAGATAGCG ATTAATAATA CACGTTTCCT AATGTGGGAT ATTGGTGGCC AAGAATCTCT 480
TCGTTCTTCC TGGAACACTT ACTATACTAA CACAGAGTTT GTAATAGTTG TTGTGGACAG 540
TACAGACAGA GAGAGGATTG CTGTAACCTAG AGAAGAACTC TATAAAATGT TAGGGCATGA 600
GGACCCAAGA AAAGCTGGAT TGCTGATTT TGCTAATAAA CAAGATGTTA AAGAATGCAT 660
GACTGTAGCA GAAATCTCCC AGTTTTGAA GCTAACTTCT ATTAAAGATC ACCAGTGGCA 720
TATCCAGGCA TGCTGTGCTC TAACTGGCGA GGGATTGTGC CAAGGACTTG AATGGATGAT 780
GTCACGACTT AAGATTAGAT GATCTCTACT GACCTCTACT CATAGATTTT GTATAAAATGA 840
AGTGCTGGAC TTTACCTGAA AGCTGCAAAA ATTAATGGTT TAGATATATT TATAATAAAC 900
TGATTTAAC ACAGTTCTATA AGAAGAAAAA TTAAGACCAC TTATTTGAAA ACAAAGATGA 960
AGTCTCACCT TCCAGTTTGC TTTCTCATTA GTTTTTTCCA AAGTAAGTTA TTGAAGCTGT 1020
GATTGACATT TTTCTCATAA TGAATCCTCT CAGGACATTG TGTAGCCTAT GGTAAGTACA 1080
AAGGGAGAGG AAGACATTTT GAATTTAAG AGCTTTATTA TCAGTTAAC CCTCCCTAGT 1140
TGAATGTTAT TTTCTCTTG TTCCATTAAG TCAGAATACA AATCAGCACA GATATTGAA 1200
TGTTTCCAAT ATTTTAAAT GTAATGTTAC TTATGAAAAG TATTTGCTT AAGGTTGTGT 1260
GTGTATTGTC TATATACCTC AAGTTCAAGT TAATGGCATT GATTTATGTT CCAGACAAAA 1320
ATAACACAAA TAATAATATC CTTCGTTATA ACCACAATGA GATAAGTATT GGCATTAGTG 1380
TTCAGTGCCA TTTTATACTT TCTCTGTG TTCTCTGTAT TGTACTAAAC AACCTCCCAA 1440
ATCGCTGAGC TGCTTGTGTTA AAAAAAAAAA 1469

- (2) INFORMATION FOR SEQ ID NO: 10 :

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 875 base pairs
 - (B) TYPE: nucleic acid
 - (C) STRANDEDNESS: single
 - (D) TOPOLOGY: linear

- (vii) IMMEDIATE SOURCE:
 - (A) LIBRARY: UCMCL5T01
 - (B) CLONE: 1528559

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 10 :

CGGGCACGCC AGGCGCCGTT GCCACCCGGG ATGGCGAGGC CCCCCGAGCGC TCCCCGCCCT 60
GCAGTCCGAG CTACGACCTC ACGGGCAAGG TGATGCTTCT GGGAGACACA GGCCTCGGCA 120
AAACATGTTT CCTGATCCAA TTCAAAGACG GGGCCTTCCT GTCCGGAACC TTCATAGCCA 180
CCGTCGGCAT AGACTTCAGG AACAAAGGTGG TGACTGTGGA TGGCGTGAGA GTGAAGCTGC 240

PF-0168-3 DIV

AGATCTGGGA CACCGCTGGG CAGGAACGGT TCCGAAGCGT CACCCATGCT TATTACAGAG 300
ATGCTCAGGC CTTGCTTCTG CTGTATGACA TCACCAACAA ATCTTCTTC GACAACATCA 360
GGGCCTGGCT CACTGAGATT CATGAGTATG CCCAGAGGGA CGTGGTGATC ATGCTGCTAG 420
GCAACAAGGC GGATATGAGC AGCGAAAGAG TGATCCGTT CGAAGACGGA GAGACCTTGG 480
CCAGGGAGTA CGGTGTTCCC TTCTGGAGA CCAGCGCCAA GACTGGCATG AATGTGGAGT 540
TAGCCTTCT GGCCATCGCC AAGGAACTGA AATACCGGGC CGGGCATCAG GCGGATGAGC 600
CCAGCTTCCA GATCCGAGAC TATGTAGAGT CCCAGAAAGAA GCGCTCCAGC TGCTGCTCCT 660
TCATGTGAAT CCCAGGGGGC AGAGAGGAGG CTCTGGAGGC ACACAGGATG CAGCCTTCCC 720
CCTCCCAGGC CTGGCTTATT CCAAGAGGCT GAGCCAATGG GGAGAAAGAT GGAGGACTCA 780
CTGCACAGCC GCTTCCCTAGC AGGGAGCTAT ACTCCAACTC CTACTTGAGT TCCTGCGGTC 840
TCCCCGCATC CACAGGGAGG GTAAAACACT TAGGG 875

(2) INFORMATION FOR SEQ ID NO: 11:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1533 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:
(A) LIBRARY: PROSTUT08
(B) CLONE: 1651593

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 11 :

CTGGCATCGC CAGATGCTGC GCACAGTCTC CGATTCCCCA TCACCAATTG GGCTGGGTC 60
TGCAGGGGCC CGGCCCCAC CAGACGGGAC TCCCCGCCCC CAATTGGCGG CGAACAGTC 120
TCCTCGCCCC AGAGTCATCT TCGGGACGCC CAGGGCCCGG GTGATTTGG GCTCGCCGCG 180
GCCCGGGGTG ATTGTTTCAT CTCCGTGGCC CGGGTGGTC GTAGCGTCTC CGAGACCGCG 240
GACTCCCGTA GGTCCCCGTG GCCCCGAGTT GTAGTCGGGA CACCCCGGCC GCGGGTGATC 300
GTCGGGTCTC CACCGGCCCG GGTGCGTGCAC GCGGATCCGG CCTCGCGGCC TTCTCAGGGC 360
GCCCTGCAAG GCCCGCAGGCA GGATGAACAT TCTGGCACCC GTGGGAGGG ATCGCGTCCT 420
GGCGGAGCTG CCCCAGTGCC TGAGGAAGGA GGCGCTTTG CACGGGCACA AAGACTTCCA 480
CCCCCGCGTC ACCTGCGCCT GCCAGGAGCA CGGACAGGC ACCGTGGCA GATTAAAGAT 540
CTCCAAGGTC ATTGTGGTGG GGGACCTGTC GGTGGGAAG ACTTGCCTCA TTAATAGGTT 600
CTGCAAAGAC ACCTTTGATA AGAATTACAA GGCCACCATT GGAGTGGACT TCGAGATGGA 660
ACGATTGAG GTGCTGGCA TTCCCTTCAG TTTGCAGCTT TGGGATACCG CTGGGCAGGA 720
GAGGTTCAAA TGCATTGCA TAAACCTACTA TAGAGGAGCT CAAGCCATCA TCATTGTCTT 780
CAACCTGAAT GATGTGGCAT CTCTGGAAACA TACCAAGCAG TGGCTGGCCG ATGCCCTGAA 840
GGAGAAATGAC CCTTCCAGTG TGCTTCTCTT CCTTGTAGGT TCCAAGAAGG ATCTGAGTAC 900
CCCTGCTCAG TATGCGCTGA TGGAGAAAGA CGCCCTCCAG GTGGCCAGG AGATGAAGGC 960
TGAGTACTGG GCAGTCTCAT CTCTCACTGG TGAGAATGTC CGAGAATTCT TCTTCCGTGT 1020
GGCAGCACTG ACCTTGAGG CCAATGTGCT GGCTGAGCTG GAGAAATCGG GGGCTCGACG 1080
CATITGGGAT GTTGTCCGCA TCAACAGTGA TGACAGCAAC CTCTACCTAA CTGCCAGCAA 1140
GAAGAAAGCCC ACATGTTGCC CATGAGGGCT GAGGAGACTG TTCAGAGACT GCCCAGCCCT 1200
AGGGCACTGT GCCACCCCTCA TTCTCCAGA GCTTGACCCC TGGACATTG CACTGACTTT 1260
ATCCAGACCA AAGAGCTGCC TCTTGGTGGC AGTATTCCCA CAGAGGGTA GCTGGATCA 1320
TGCTAGTCAC TTCTGCCCC CAGGCACCGT GCCAAAGACT GGATGCCCT TACTCCTCAG 1380
GGGACTGTCC AGGGCGCCCA GTGGTAGTGA GGGAGAGTGT CTCTGTTCTT TTGCTCAGCC 1440
TGCTGGGCC TTTGTGTTTG AGGATGCTTA ATGATTCCAG CCTCTCACTG TGCCTTATGC 1500
ATTAAAATTT CTTGTTACG AGCAAAAAAA AAA 1533

400514986-041502

(2) INFORMATION FOR SEQ ID NO: 12:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1173 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: BLADNOT05
- (B) CLONE: 1673056

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 12 :

ATATTTTAGA AATCTAGCAT TTTAGAACATT TTGGGCATT TTAAATACAG GTGAATATTT 60
 GAATTTGGTT TGACACAAAA TACAGAACATT ATGAAGCATG CAGATGTTG GCGTGTGCC 120
 CGAACGACCC TCTACTCTGT CCTCTGCACC CACCCCTTGC GCCTCTGCGT CAGCCACAGC 180
 TGCCCCGGGA GCGAGTTCTC CTGAGGCCTC GGCTGTGCTG ACTCTAGGGC AGCGTGAGGG 240
 TGGTTGTCAG CTGTGAAGGT GCCACTTACA CACTAAGTCC TCCTTCCTTG TGGAGGGAAG 300
 GGCTCAAGTA GCAAATATTG GAGCCCCCGC TTGGTGCTGG GAGCTGTGAC AGGCAGCTCC 360
 TGAAGAAGCA GTTTAATTGG AACCAAGTGAC CATCTAAAAC TGTTTGTACT CTAAACCAGA 420
 TTTTACAGAA ATATTGGAAT CATAACCTTA TACTTGATT TTTCATTTA GATAGTTAGG 480
 CGTAAAGGAA GCCTCCTGAG GGTCTGGTCT GATCCTCCTG ATCCTTGAAG AGCTTCCAGC 540
 ATCATTCTCC CTTCATGCTC CCCATTTCA TAAGTAAC TGCGCTTGAC ATGCTGGTT 600
 TGGTTTGGGA GCCCTCTGAC AAACTGAAAG GGTGGATCAG GAAGCGTCTG ACCACACCAC 660
 TGGTAGCTGG ACAAGAAGAT TATGACAGAT TACGGCACCT ATCCTATCCG CAAACAGTTG 720
 GAGAAACGTA CGGTAAGGAT ATAACCTCCC GGGGCAAAGA CATGCCGATT GCCGATGTGT 780
 TCTTAATTG CTTTCCCTT GTGAGTCTTG CATCATTGAA AAATGTCCGT GCAAAGTGGT 840
 ATCCTGAGGT GCGGCACAC TGTCACAAACA CTCCCATCAT CCTAGTGGGA ACTAAACTTG 900
 ATCTTAGGGA TGATAAAAGAC ACGATCGAGA AACTGAAGGA GAAGAAGCTG ACTCCCATCA 960
 CCTATCCGCA GGGCTAGCC ATGGCTAAGG AGATTGGTGC TGTAAAATAC CTGGAGTGCT 1020
 CGGCGCTCAC ACAGCGAGGC CTCAGACAG TGTGGACGA AGCGATCCGA GCAGTCATCT 1080
 GCCCGCCTCC CGTGAAGAAG AGGAAGAGAA AATGCCCTGAT GTTGTAAATG TCTCAGCCCC 1140
 TCGTTCTTGT CCTGCCCTTG GACCTTTGC GTC 1173

(2) INFORMATION FOR SEQ ID NO: 13:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 803 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: OVARTUT10
- (B) CLONE: 2703745

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 13 :

CAGCACTCTC GCCCCAGACA GACCTGGTAG ATGACAACGC TAAATCTTT AGCTCACAGA 60
 AGGCTTACAA GATTGTACTT GCTGGGGACG CTGCAGTGGG GAAGTCTAGT TTCCTCATGG 120
 AGACTTTGCA AGAATGAATT TCGAGAAAAT ATAAGCGCCA CCCTGGGAGT TGATTTCAA 180
 ATGAAAACCC TCATTGTGGA TGGAGAACGA ACAGTTCTGC AGCTCTGGGA TACAGCTGGT 240

CAGGAGAGAT TCAGAAAGTAT TGCCAAGTCT TACTTCAGAA AGGCAGATGG TGTTTGCTG 300
 CTGTATGATG TTACATGTGA GAAAAGCTT CTTAACATAC GAGAATGGGT AGATATGATT 360
 GAGGATGCAG CCCATGAGAC TGTTCCCATT ATGCTGGTAG GAAACAAGGC TGACATTCTG 420
 GACACTGCTG CTACAGAGGG ACAAAAATGT GTCCCAGGGC ACTTTGGAGA GAAACTGGCC 480
 ATGACGTATG GGGCATTATT CTGTGAAACA AGTGCCAAAG ATGGTTCTAA CATAGTGGAG 540
 GCTGTTCTGC ACCTTGCTCG AGAAAGTCAA AAGAGAACTG ACAAGGATGA CAGCAGATCC 600
 ATTACCAATC TAACCAGGGAC CAATTCCAA AAGTCACCCAG AGATGAAGAA TTGTTGCAAT 660
 GGCTAAATCC CAAACATCCT TGGCCTGTGA AGTCTTCATT TCCAGAATAC TGAATTGTG 720
 TGACTTATTG GGCCTTAAC AGAGTGGCAC ATCCTACTGA CACTGTCCTA TGGAGAGTTA 780
 CAGTGCAGGA AACCTGAACC CAG 803

(2) INFORMATION FOR SEQ ID NO: 14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 890 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PENCNOT06
- (B) CLONE: 3440519

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 14 :

GTCGCCATGT CCTCGGTGTT TGGAAAACCC CGCCGCGGC GCGGGCCTCA GAGCGCGCCC 60
 CTCGAGGTCA ACCTGGCCAT CCTGGGGCGC CGCGGGGCTG GCAAGTCTGC CCTGACCGTG 120
 AAGTTTCTGA CCAAGAGGTT TATCAGTGAA TATGACCCCA ACTTGGAGGA CACCTACAGC 180
 TCCGAGGAGA CTGTGGACCA CCAGCCTGTC CACCTGAGGG TCATGGACAC TGCAGACCTG 240
 GACACCCCCA GGAACCTGCGA GCGCTACCTG AACTGGGCC ATGCCTTCTC GGTGGTGTAC 300
 AGCGTCGACA CCCGCCAGAG CTTTGATAGC AGCAGCAGCT ACCTGGAGCT GCTTGCCTTG 360
 CACGCGAAGG AGACACAGCG CAGCATTCCCT GCCCTGCTGC TGGGCAACAA GCTGGACATG 420
 GCTCAGTACA GGCAAGTCAC CAAGGCAGAG GGTGTGGCTT TGGCAGGCAG GTTTGGGTGC 480
 CTGTTTTCTCG AGGTCTCTGC CTGTCTGGAC TTTGAGCAGC TGCAAGCATGT CTTCCACGAG 540
 GCAGTGCAG AGGCACGGCG GGAGCTGGAG AAGAGCCCCC TGACCCGGCC CCTCTTCATC 600
 TCCGAGGAGA GGGCCCTGCC CCACCAGGCC CCGCTCACTG CGCGGCATGG GCTGGCCAGC 660
 TGCACCTTCA ACACGCTCTC CACCATCAAC CTGAAGGAGA TGCCCACTGT GGCCCAGGCC 720
 AAGCTGGTCA CCGTGAAGTC ATCCCAGGCC CAGAGCAAGC GCAAGGCGCC TACCCCTGACT 780
 CTCCTGAAGG GCTTCAAGAT CTTCTGAGGC CCCCTCCCCA GGAAGCCTAG GCTCGGTGGC 840
 TGGACAGGAC TGCAGCAGGA CAGGGACTGG CTTCTCACCA CCAGCCTTTC 890

2025 RELEASE UNDER E.O. 14176